

FIGURE 1

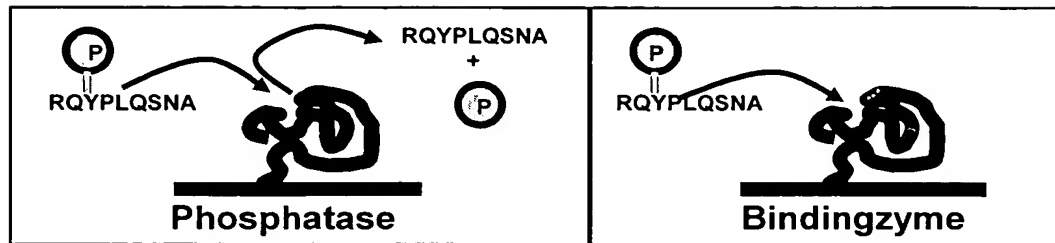


FIGURE 2

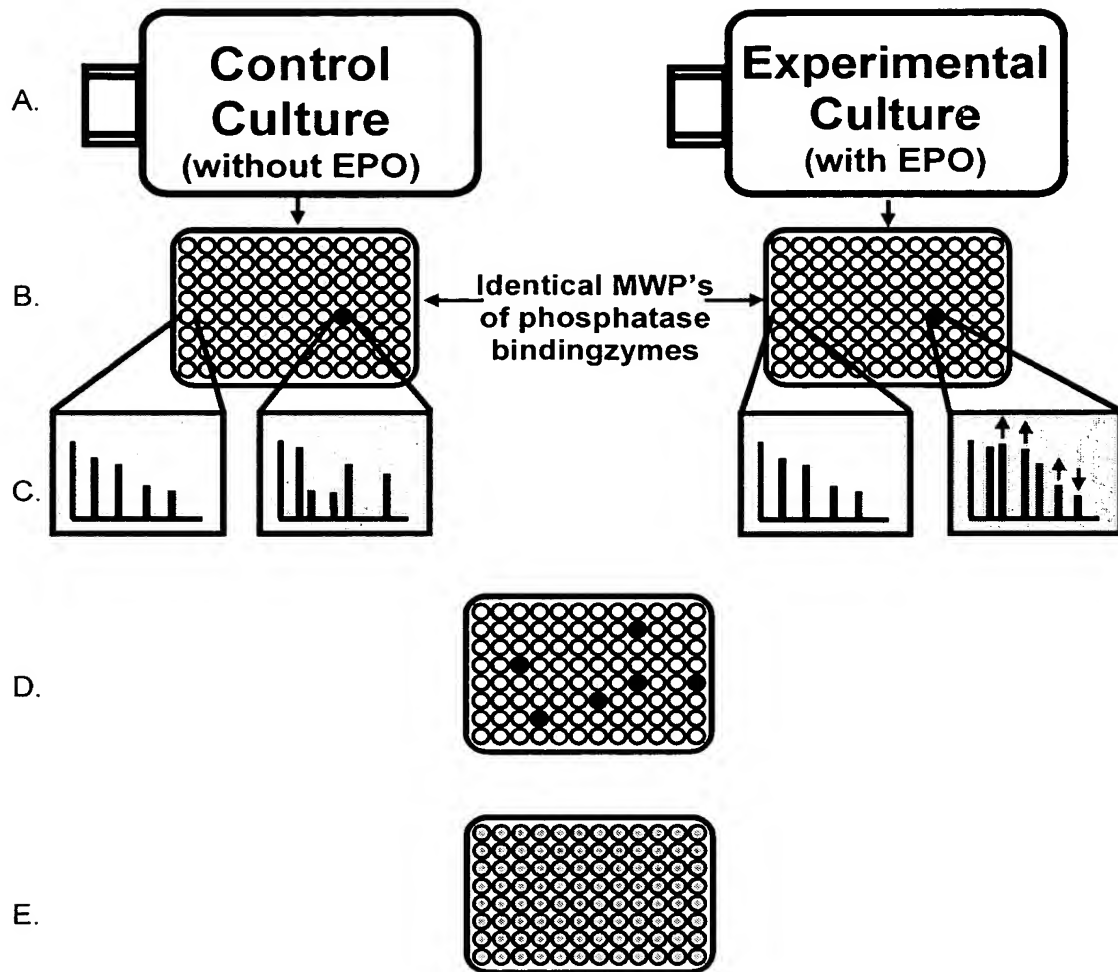


FIGURE 3A

Bindingzyme	Gene ID	Variant	Peptide Length	Shortest	RefSeq ID	Aliases	Isoforms	Comment
1	PTPRC	1	1304		<u>NM_002838</u>		1	Regulates T- and B-cell signalling.
		2	1143		<u>NM_080921</u>		2	Can activate Src family kinases and inhibit JAK kinases.
		3	1256	34	<u>NM_080922</u>	LCA, LY5, B220, CD45, T200, GP180	3	
		4	34		<u>NM_080923</u>		4	
2	ACP1	1	70		<u>NM_177554</u>		a	PTP and acid phosphatase
		2	158	70	<u>NM_007099</u>	HAAP, MGC3499	b (Bs)	
		3	158		<u>NM_004300</u>		c, (Bf)	
		1	167		<u>NM_003479</u>	HH13, OV-1, PRL2, HH7-2, PRL-2,	1	Cancer Panel; C-terminal prenylation motif
3	PTP4A2	2	167	82	<u>NM_080391</u>	PTP4A, HU-PP-1,	1	
		3	82		<u>NM_080392</u>	PTPCAAX2, ptp-IV1a, ptp-IV1b	2	
		1	173	148	<u>NM_032611</u>	PRL3, PRL-3, PRL-R	1	Prenylated, All affect
		2	148		<u>NM_007079</u>		2	
4	PTP4A3	1	173		<u>NM_003463</u>	HH72, PRL1, PRL-1, PTPCAAX1, PTP(CAAX1)		Cancer Panel; Prenylated
		2	173		<u>NM_003463</u>	PTPLA		adult & fetal heart
5	PTPLA	1	288	288	<u>NM_014241</u>		1	Substrates: EGFR & Shc
		2	415		<u>NM_002828</u>	PTPT, TCPTP, TC-PTP, TCELLPTP	2	
		3	387	353	<u>NM_080422</u>		3	
		3	353		<u>NM_080423</u>			TCR signalling; MAPK
6	PTPN2	1	360		<u>NM_002832</u>	LPTP, HEPTP,	1	
		2	399	360	<u>NM_080588</u>	PTPNI, BPTP-4, LC-PTP	2	
		3	360		<u>NM_080589</u>		1	
		3	1216		<u>NM_030667</u>		a	Variants exhibit tissue-specific expression.
7	PTPN7	1	1188		<u>NM_002848</u>		b	
		2	405		<u>NM_030669</u>	PTPU2, GLEPP1,	c	Isoforms c, d are candidates for the Cancer Panel.
		3	377	377	<u>NM_030668</u>	PTP-U2	d	
		4	405		<u>NM_030671</u>		c	
8	PTPRO	5	405		<u>NM_030671</u>		c	
		6	377		<u>NM_030670</u>		d	

FIGURE 3B

Bindingzyme	Gene ID	Variant	Peptide Length	Shortest	RefSeq ID	Aliases	Isoforms	Comment
10	PTEN		403		<u>NM_000314</u>	BZS, MHAM, TEP1, MMAC1, PTEN1		Cancer Panel
11	PTPRR	1	657		<u>NM_002849</u>	PTPRQ, EC-PTP,	1	Neuronal growth
		2	412	412	<u>NM_130846</u>	PCPTP1, PTP-SL, PTPBR7	2	and differentiation
12	PTPN1		435	435	<u>NM_002827</u>	PTP1B		Diabetes
								In most tissues.
13	PTPN11	1	593	460	<u>NM_002834</u>	CFC, NS1, SHP2, BPTP3, PTP2C, SHP-2, PTP-1D, SH-PTP2, SH-PTP3	1	Mutations associated w/Noonan syndrome.
		2	460		<u>NM_080601</u>		2	Under Review
14	PTPN18		460	460	<u>NM_014369</u>	BDP1		Cancer Panel
15	PTPN5		565	565	<u>NM_032781</u>	STEP, PTPSTEP, FLJ14427		Provisional RefSeq
16	PTPN9		593	593	<u>NM_002833</u>	MEG2		Phagocytosis
		1	595		<u>NM_002831</u>	HCP, HCPH, SHP-1,	1	
17	PTPN6	2	597	595	<u>NM_080548</u>	HPTP1C, PTP-1C,	2	Hematopoietic cells
		3	624		<u>NM_080549</u>	SHP-1L, SH-PTP1	3	
		1	700		<u>NM_006504</u>		1	RAS related
								pathways; SATA
18	PTPRE	2	642	642	<u>NM_130435</u>	PTPE, HPTPE, R-PTP-EPSILON	2	signaling; activation of voltage-gated K+ channels
		1	807		<u>NM_015967</u>		1	Primarily Lymphoid
19	PTPN22	2	691	691	<u>NM_012411</u>	LYP, Lyp1, Lyp2	2	tissues. Associates with CBL
20	PTPN12		780	780	<u>NM_002835</u>	PTPG1, PTP-PEST		Cancer Panel

FIGURE 3C

Bindingzyme	Gene ID	Variant	Peptide Length	Shortest	RefSeq ID	Aliases	Isoforms	Comment
21	PTPN3		913	913	<u>NM 002829</u>	PTPH1		Band 4.1 domain. P97 is a substrate. Regulated by adaptor protein 14-3-3 beta.
22	PTPN4		926	926	<u>NM 002830</u>	PTPMEG, PTPMEG1		Band 4.1 domain
23	PTPRN		979	979	<u>NM 002846</u>	IA2, IA-2, ICA512, R-PTP-N, IA-2/PTP		Diabetes
		1	1015		<u>NM 002847</u>	IAR, ICAAR,	1	
24	PTPRN2	2	998	986	<u>NM 130842</u>	PTPRP, PHOGRIN,	2	Diabetes
		3	986		<u>NM 130843</u>	IA-2beta, KIAA0387, IAR PTPRP	3	
25	PTPRH		1118	1118	<u>NM 002842</u>	SAP-1		Cancer Panel
26	PTPN21		1174	1174	<u>NM 007039</u>	PTPD1, PTPRL10		BMX/ETK interaction
27	PTPN14		1187	1187	<u>NM 005401</u>	PEZ, PTP36		Band 4.1 domain
28	PTPRJ		1337	1337	<u>NM 002843</u>	DEP1, SCC1, CD148, HPTPeta, R-PTP-ETA		(-) regulator of T-cell signalling
		1	1436		<u>NM 133178</u>	FMI, PTP, PCP-2,	1	MAM domain.
		2	1440		<u>NM 133177</u>	PTP-J, PTPRO,	2	Neural development.
29	PTPRU	3	1446	1436	<u>NM 005704</u>	PTPU2, GLEPP1, PTP-PI, PTPPSI, hPTP-J, R-PTP-PSI, pi R-PTP-Psi	3	Regulated by PMA in Jurkat cells.
30	PTPRK		1440	1440	<u>NM 002844</u>	R-PTP-kappa		MAM domain. Candidate for Cancer Panel
31	PTPRG		1445	1445	<u>NM 002841</u>	PTPG, HPTPG, RPTPG, R-PTP-GAMMA		Cancer Panel. CAH domain.

FIGURE 3D

Bindingzyme	Gene ID	Variant	Peptide Length	Shortest	RefSeq ID	Aliases	Isoforms	Comment
32	PTPRM		1452	1452	<u>NM_002845</u>	RPTPM, RPTPU, PTPRL1, hR-PTPu, R-PTP-MU		MAM domain
33	PTPRT	1	1463	1463	<u>NM_133170</u>	RPTPrho, KIAA0283	1	MAM domain.
		2	1444		<u>NM_007050</u>		2	Central nervous system.
34	PTPRD	1	1912		<u>NM_002839</u>	HPTP, PTPD,	1	
		2	1899		<u>NM_130391</u>	HPTPD, HPTP-	2	Neuron growth,
		3	1903	1501	<u>NM_130392</u>	DELTA, R-PTP-	3	axon guidance
		4	1501		<u>NM_130393</u>	DELTA	4	
35	PTPRS	1	1948		<u>NM_002850</u>		1	
		2	1910		<u>NM_130854</u>	PTPSIGMA	2	Axonogenesis and
		3	1501	1501	<u>NM_130853</u>		3	nerve repair.
		4	1505		<u>NM_130855</u>		4	
36	PTPN23		1636	1636	<u>NM_015466</u>	HDPTP, HD-PTP, KIAA1471, DKFZP564F0923		Predicted RefSeq
37	PTPRF	1	1897	1888	<u>NM_002840</u>	LAR	1	Diabetes
		2	1888		<u>NM_130440</u>		2	Implicated in cell adhesion, neurite growth, and neuronal differentiation.
38	PTPRB		1997	1997	<u>NM_002837</u>	PTPB, HPTPB, HPTP-BETA, R-PTP-BETA		Potential role in Fas-mediated programmed cell death; Rho signaling pathway
39	PTPN13	1	2485		<u>NM_080683</u>	PNP1, FAP-1,	1	
		2	2466		<u>NM_006264</u>	PTP1E, PTP1L1,	2	
		3	2294	2294	<u>NM_080684</u>	PTPLE, PTP-BL,	3	
		4	2490		<u>NM_080685</u>	PTP-BAS	4	

FIGURE 4A
Candidate PTPS

Phosphatase	Genbank accession number	Coding sequence (bp)	Isolated from	MW wildtype (KDa)	MW fusion proteins GST /MBP	Mutant 1	Mutant 2	Double Mutant
He PTP variant 1	NM 002832	1,083 bp	Jurkat	40.5	66.5 / 82.5	D257A	Q335A	D257A Q335A
He PTP variant 2	NM 080588	1,200 bp	Jurkat	45.0	71.0 / 87.0	D296A	Q374A	D296A Q374A
MEG2	NM 002833	1,782 bp	Jurkat	68.0	94.0 / 110.0	D470A	Q559A	D470A Q559A
PTEN	NM 000314	1,212 bp	Jurkat	47.2	73.2 / 89.2	D92A	C124A	D92A C124A
SHP2 variant 1	NM 002834	1,782 bp	Jurkat	68.1	94.1 / 110.2	D425A	Q526A	D425A Q526A
SHP2 variant 2	NM 080601	1,383 bp	Jurkat	52.8	78.8 / 94.8	D425A	—	D425A —
TCPTP variant 1	NM 002828	1,248 bp	Jurkat	48.5	74.5 / 90.5	D182A	Q260A	D182A Q260A
PEST*	NM 002835	1,041 bp	K562	40.6	66.6 / 82.6	D199A	Q278A	D199A Q278A
PTP1B	M33689	1,308 bp	K562	50.0	76.0 / 92.0	D181A	Q262A	D181A Q262A

FIGURE 4B
PCR and Mutagenesis Primers

Phosphatase	PCR forward	PCR reverse	Mutant 1	Mutant 2
HePTP Variant 1	GAC GGA TCC ATG GTC CAA GCC CAT GGG	CAG GTC GAC TCA GGG GCT GGG TTC CTC	G GCC TGG CCA GGC CAT CAG ACA CCA	A GGG GGG ATG ATC GCG ACG GCA GAG CAG T
HePTP variant 2	GAC GGA TCC ATG GGA GCC TCC TTC TGG	CAG GTC GAC TCA GGG GCT GGG TTC CTC A	G GCC TGG CCA GGC CAT CAG ACA CCA	A GGG GGG ATG ATC GCG ACG GCA GAG CAG T
MEG2	ATA GAA TTC ATG GAG CCC GCG ACC GC	ATA TCT AGA TTA CTG ACT CTC CAC GGC CAG	TTG AGC TGG CCA GGC TAT GGT GTC CCT TC	G GCC TTC AGC ATC GCG ACC CCT GAG CAG T
PTEN	GAC GAA TTC ATG ACA GCC ATC ATC AAA GAG	CAG TCT AGA TCA GAC TTT TGT AAT TTG TGT ATG C	CA CAA TAT CCT TTT GAA GCC CAT AAC CCA CCA CAG	T CAT GTT GCA GCA ATT CAC GCT AAA GCT GGA AAG GGA CG
SHP2 variant 1	GAC GAA TTC ATG ACA TCG CGG AGA TGG	CAG TCT AGA TCA TCT GAA ACT TTT CTG CTG TTG	G ACC TGG CCG GGC CAC GCC GTG C	C CAG CAT TAT ATT GAA ACA CTA GCG CGC AGG ATT GAA GAA GAG
SHP2 variant 2	GAC GAA TTC ATG ACA TCG CGG AGA TGG	CAG TCT AGA TCA CCT GCA GTG CAC CAC	G ACC TGG CCG GGC CAC GCC GTG C	—
TCPTP variant 1	GAC GAA TTC ATG CCC ACC ACC ATC GAG	CA GGT CGA CAT TGT TTA TAG GGC ATT TTG CT G	T TAT ACT ACC TGG CCA GCT TTT GGA GTC CCT GAA T	AC CGA ATG GGT CTT ATT GCG ACC CCA GAT CAA CTG AG
PEST	GAC GGA TCC ATG GAG CAA GTC GAG ATC CTG	CAG GTC GAC TCA TTC AAC AAG GCA ACT GCG GG	TAT GTG AAC TGG CCVA GGC CAT GAT GTT CCT TCA TC	CA CAA AGG CAT TCT GCA GTA GCA ACA AAG GAG CAA TAT GAA CT
PTP1B	GAC GGA TCC ATG GAG ATG GAA AAG GAG TTC G	CAG GTC GAC CTA TGT GTT GCT GTT GAA CAG G	T ACC ACA TGG CCT GGC TTT GGA GTC CCT G	G ATG GGG CTG ATC GCG ACA GCC GAC CAG C

FIGURE 5

